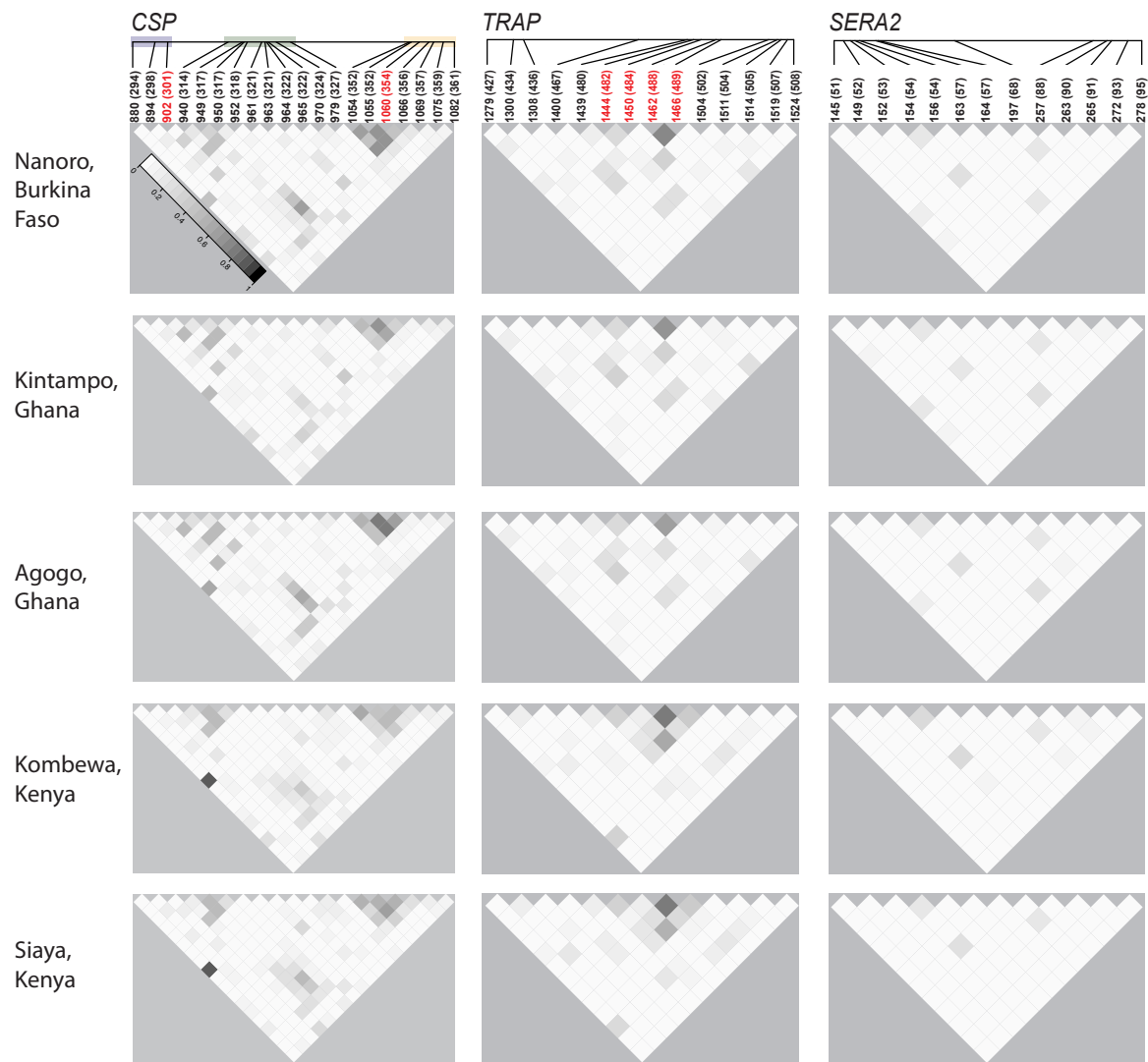
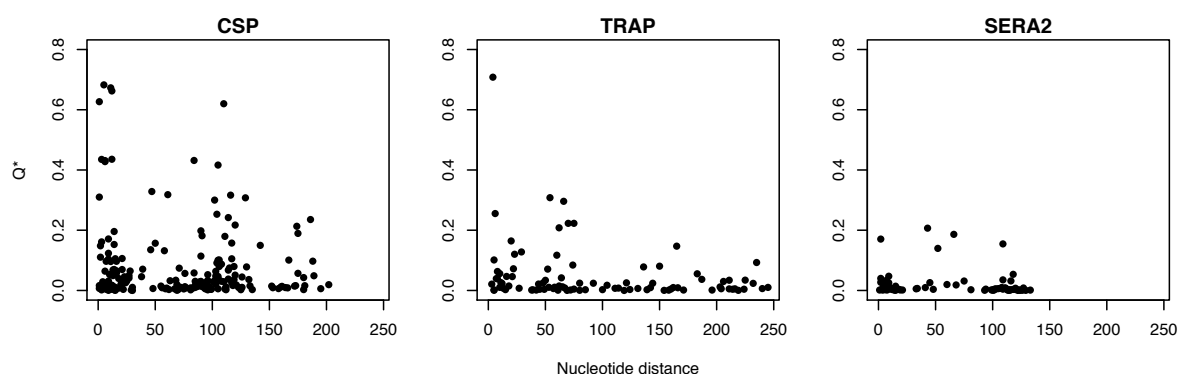


## Supplementary Material

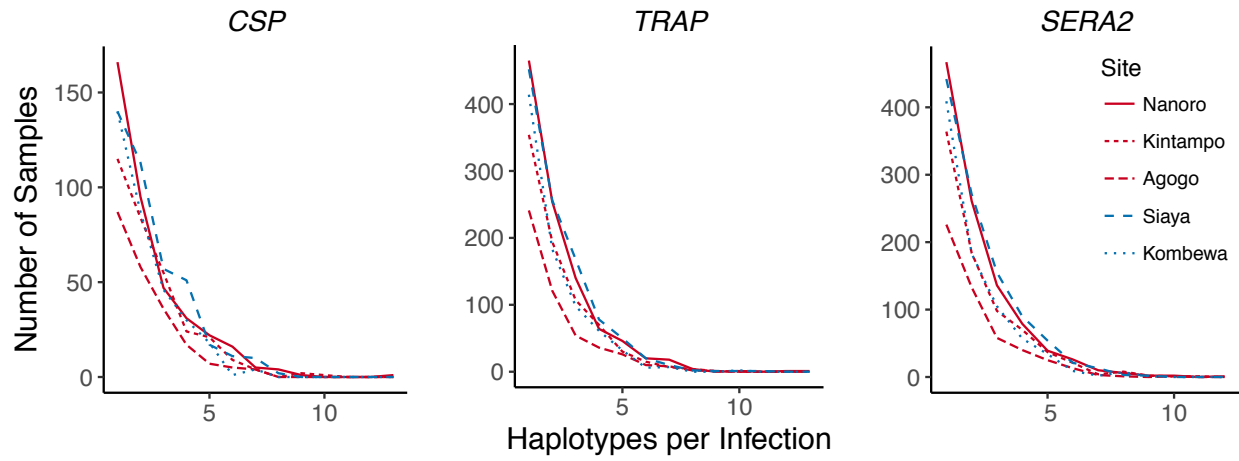
Early *et al.* Host-mediated selection impacts the diversity of *Plasmodium falciparum* antigens within infections.



**Supplementary Figure 1. LD plots for nucleotides within the *CSP*, *TRAP*, and *SERA2* amplicon regions for each of the five study sites.** LD between polymorphic nucleotides was calculated as  $Q^*$ , an extension of  $r^2$  that allows for multiple alleles per site. Corresponding amino acid positions are in parentheses. Positions marked in red showed evidence for altered intra-host diversity at the amino acid level. For *CSP*, shading marks the positions within the DV10 (blue), Th2R (green), and Th3R (yellow) epitope regions. Only nucleotide positions with a major allele frequency  $<0.98$  were included in the analysis.



**Supplementary Figure 2. Plots of LD ( $Q^*$ ) decay with nucleotide distance for the *CSP*, *TRAP*, and *SERA2* amplicon regions.** LD between polymorphic nucleotides was calculated as  $Q^*$ , an extension of  $r^2$  that allows for multiple alleles per site.



**Supplementary Figure 3. Number of haplotypes sequenced per infection for each amplicon region.**